

- 1 -

## SEQUENCE LISTING

&lt;110&gt; THE UNIVERSITY OF QUEENSLAND

&lt;120&gt; A NOVEL PLANT PROMOTER AND USES THEREFOR

&lt;130&gt; 2209376/EJH

&lt;140&gt;

&lt;141&gt;

&lt;150&gt; PP5572

&lt;151&gt; 1998-08-31

&lt;160&gt; 9

&lt;170&gt; PatentIn Ver. 2.0

&lt;210&gt; 1

&lt;211&gt; 1923

&lt;212&gt; DNA

&lt;213&gt; Plant

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (88) .. (1539)

&lt;400&gt; 1

atcctctctc ccacttactt cgatttcac aattccaata aactcaacac actttttttac 60

actccacact ctaaccacat acaccat atg ggt ttc aag gcc atg gac caa act 114  
Met Gly Phe Lys Ala Met Asp Gln Thr  
1 5ccc ttg ttg tcc aag atg gct att ggg gat gga cat ggc gaa tca tcc 162  
Pro Leu Leu Ser Lys Met Ala Ile Gly Asp Gly His Gly Glu Ser Ser  
10 15 20 25cca tac ttt gat gga tgg aag gct tat gat caa aac ccc ttt cat ccc 210  
Pro Tyr Phe Asp Gly Trp Lys Ala Tyr Asp Gln Asn Pro Phe His Pro  
30 35 40aca gat aat cct aac ggt gtt atg caa atg ggt ctt gct gag aat cag 258  
Thr Asp Asn Pro Asn Gly Val Met Gln Met Gly Leu Ala Glu Asn Gln  
45 50 55

- 2 -

ctt acc tct gat ttg gtt gaa gat tgg ata ctg aac aac cct gaa gcc 306  
 Leu Thr Ser Asp Leu Val Glu Asp Trp Ile Leu Asn Asn Pro Glu Ala  
 60 65 70

tcc att tgc act cca gaa gga ata aat gat ttc agg gcc ata gct aac 354  
 Ser Ile Cys Thr Pro Glu Gly Ile Asn Asp Phe Arg Ala Ile Ala Asn  
 75 80 85

ttt cag gat tat cat ggt ctg gcc gag ttc aga aat gct gtg gct aaa 402  
 Phe Gln Asp Tyr His Gly Leu Ala Glu Phe Arg Asn Ala Val Ala Lys  
 90 95 100 105

ttt atg gct aga aca agg gga aac aga atc acg ttt gac cct gac cgt 450  
 Phe Met Ala Arg Thr Arg Gly Asn Arg Ile Thr Phe Asp Pro Asp Arg  
 110 115 120

att gtc atg agc ggt gga gcc acc gga gca cac gaa gtc act gcc ttt 498  
 Ile Val Met Ser Gly Gly Ala Thr Gly Ala His Glu Val Thr Ala Phe  
 125 130 135

tgt ttg gca gat ccc ggc gag gca ttc tta gtg ccc att ccc tat tat 546  
 Cys Leu Ala Asp Pro Gly Glu Ala Phe Leu Val Pro Ile Pro Tyr Tyr  
 140 145 150

cca ggc ttt gac cgg gat ttg agg tgg aga aca gga gtt aaa ctt gtt 594  
 Pro Gly Phe Asp Arg Asp Leu Arg Trp Arg Thr Gly Val Lys Leu Val  
 155 160 165

cca gtt atg tgc gat agc tca aat aat ttc gtg ttg aca aag gaa gca 642  
 Pro Val Met Cys Asp Ser Ser Asn Asn Phe Val Leu Thr Lys Glu Ala  
 170 175 180 185

ttg gaa gat gcc tat gag aaa gca aga gag gat aac atc aga gta aag 690  
 Leu Glu Asp Ala Tyr Glu Lys Ala Arg Glu Asp Asn Ile Arg Val Lys  
 190 195 200

ggt tta ctg atc acc aat cca tca aat cca tta ggc aca atc atg gac 738  
 Gly Leu Leu Ile Thr Asn Pro Ser Asn Pro Leu Gly Thr Ile Met Asp  
 205 210 215

aga aag aca ctg aga acc gtg gtg agc ttc atc aat gag aag cgt atc 786  
 Arg Lys Thr Leu Arg Thr Val Val Ser Phe Ile Asn Glu Lys Arg Ile  
 220 225 230

cac ctt gta tgt gat gaa ata tat gct gca aca gtt ttc agc caa ccc 834  
 His Leu Val Cys Asp Glu Ile Tyr Ala Ala Thr Val Phe Ser Gln Pro

- 3 -

235	240	245	
ggt ttc ata agc ata gct gag ata tta gag gat gaa aca gac ata gag			882
Gly Phe Ile Ser Ile Ala Glu Ile Leu Glu Asp Glu Thr Asp Ile Glu			
250	255	260	265
tgt gac cgc aac ctc gta cac att gtt tat agt ctt tca aag gac atg			930
Cys Asp Arg Asn Leu Val His Ile Val Tyr Ser Leu Ser Lys Asp Met			
	270	275	280
ggg ttc cct ggc ttc aga gtc ggc atc ata tac tct tac aat gat gct			978
Gly Phe Pro Gly Phe Arg Val Gly Ile Ile Tyr Ser Tyr Asn Asp Ala			
	285	290	295
gtg gtt aat tgt gca cgc aaa atg tca agc ttt gga ttg gtg tca aca			1026
Val Val Asn Cys Ala Arg Lys Met Ser Ser Phe Gly Leu Val Ser Thr			
	300	305	310
cag act cag tat ctt tta gca tgc atg cta aat gat gat gag ttt gtg			1074
Gln Thr Gln Tyr Leu Leu Ala Ser Met Leu Asn Asp Asp Glu Phe Val			
	315	320	325
gag agg ttt ctg gca gag agt gca aag agg ttg gct caa agg ttc agg			1122
Glu Arg Phe Leu Ala Glu Ser Ala Lys Arg Leu Ala Gln Arg Phe Arg			
	330	335	340
gtt ttc act ggg ggg ttg gcc aaa gtt ggc ata aag tgc ttg caa agc			1170
Val Phe Thr Gly Gly Leu Ala Lys Val Gly Ile Lys Cys Leu Gln Ser			
	350	355	360
aat gct ggt cta ttt gtg tgg atg gat tta agg caa ctt ctc aaa aag			1218
Asn Ala Gly Leu Phe Val Trp Met Asp Leu Arg Gln Leu Leu Lys Lys			
	365	370	375
cca act ttc gac tct gaa acg gag ctt tgg aaa gtt atc att cat gaa			1266
Pro Thr Phe Asp Ser Glu Thr Glu Leu Trp Lys Val Ile Ile His Glu			
	380	385	390
gtt aag atc aat gtt tca cct ggc tat tcc ttc cat tgc act gag cca			1314
Val Lys Ile Asn Val Ser Pro Gly Tyr Ser Phe His Cys Thr Glu Pro			
	395	400	405
ggg tgg ttt agg gtg tgc tat gcc aac atg gat gat atg gct gtg caa			1362
Gly Trp Phe Arg Val Cys Tyr Ala Asn Met Asp Asp Met Ala Val Gln			
	410	415	420
			425

- 4 -

att gct ttg caa cga atc cgc aac ttt gtg ctt caa aac aag gag gtc 1410  
 Ile Ala Leu Gln Arg Ile Arg Asn Phe Val Leu Gln Asn Lys Glu Val  
 430 435 440

gtg gtg tct aat aag aaa cat tgt tgg cac agt aac ttg agg ctg agc 1458  
 Val Val Ser Asn Lys Lys His Cys Trp His Ser Asn Leu Arg Leu Ser  
 445 450 455

ctc aaa acc aga agg ttt gat gat atc acc atg tca cct cac tct ccc 1506  
 Leu Lys Thr Arg Arg Phe Asp Asp Ile Thr Met Ser Pro His Ser Pro  
 460 465 470

cta cct cag tca cct atg gtt aaa gcc aca aat tgagtttgca tattcctctg 1559  
 Leu Pro Gln Ser Pro Met Val Lys Ala Thr Asn  
 475 480

aatcgtttag aagaagtaac tgatatgtga agattacttg gttcttttat ttgttatttt 1619

gagaaggtag ataagtgtg gatttggtct ttggaacagc aataacagga aattcctgat 1679

gttggtttgt gatcggtac acaatccagt gtcttacaag ttgtgctgct tcatgcacgc 1739

cccttcaatc ttaggggcat tttttctttt ttcacttacc aaagggtcaa ggtgaaaaaa 1799

gtttatagag tctgtaagt tattggttta tcagaagagt ccaaaagatg tctgtaattct 1859

gctactgaaa ttgtaacttt caattatgaa taaattgtta ataaaggtct tcaaattcat 1919

ttcc 1923

<210> 2

<211> 484

<212> PRT

<213> Plant

<400> 2

Met Gly Phe Lys Ala Met Asp Gln Thr Pro Leu Leu Ser Lys Met Ala  
 1 5 10 15

Ile Gly Asp Gly His Gly Glu Ser Ser Pro Tyr Phe Asp Gly Trp Lys  
 20 25 30

Ala Tyr Asp Gln Asn Pro Phe His Pro Thr Asp Asn Pro Asn Gly Val  
 35 40 45

- 5 -

Met Gln Met Gly Leu Ala Glu Asn Gln Leu Thr Ser Asp Leu Val Glu  
 50 55 60

Asp Trp Ile Leu Asn Asn Pro Glu Ala Ser Ile Cys Thr Pro Glu Gly  
 65 70 75 80

Ile Asn Asp Phe Arg Ala Ile Ala Asn Phe Gln Asp Tyr His Gly Leu  
 85 90 95

Ala Glu Phe Arg Asn Ala Val Ala Lys Phe Met Ala Arg Thr Arg Gly  
 100 105 110

Asn Arg Ile Thr Phe Asp Pro Asp Arg Ile Val Met Ser Gly Gly Ala  
 115 120 125

Thr Gly Ala His Glu Val Thr Ala Phe Cys Leu Ala Asp Pro Gly Glu  
 130 135 140

Ala Phe Leu Val Pro Ile Pro Tyr Tyr Pro Gly Phe Asp Arg Asp Leu  
 145 150 155 160

Arg Trp Arg Thr Gly Val Lys Leu Val Pro Val Met Cys Asp Ser Ser  
 165 170 175

Asn Asn Phe Val Leu Thr Lys Glu Ala Leu Glu Asp Ala Tyr Glu Lys  
 180 185 190

Ala Arg Glu Asp Asn Ile Arg Val Lys Gly Leu Leu Ile Thr Asn Pro  
 195 200 205

Ser Asn Pro Leu Gly Thr Ile Met Asp Arg Lys Thr Leu Arg Thr Val  
 210 215 220

Val Ser Phe Ile Asn Glu Lys Arg Ile His Leu Val Cys Asp Glu Ile  
 225 230 235 240

Tyr Ala Ala Thr Val Phe Ser Gln Pro Gly Phe Ile Ser Ile Ala Glu  
 245 250 255

Ile Leu Glu Asp Glu Thr Asp Ile Glu Cys Asp Arg Asn Leu Val His  
 260 265 270

Ile Val Tyr Ser Leu Ser Lys Asp Met Gly Phe Pro Gly Phe Arg Val  
 275 280 285

Gly Ile Ile Tyr Ser Tyr Asn Asp Ala Val Val Asn Cys Ala Arg Lys

- 6 -

290                                      295                                      300  
 Met Ser Ser Phe Gly Leu Val Ser Thr Gln Thr Gln Tyr Leu Leu Ala  
 305                                      310                                      315                                      320  
 Ser Met Leu Asn Asp Asp Glu Phe Val Glu Arg Phe Leu Ala Glu Ser  
                                     325                                      330                                      335  
 Ala Lys Arg Leu Ala Gln Arg Phe Arg Val Phe Thr Gly Gly Leu Ala  
                                     340                                      345                                      350  
 Lys Val Gly Ile Lys Cys Leu Gln Ser Asn Ala Gly Leu Phe Val Trp  
                                     355                                      360                                      365  
 Met Asp Leu Arg Gln Leu Leu Lys Lys Pro Thr Phe Asp Ser Glu Thr  
                                     370                                      375                                      380  
 Glu Leu Trp Lys Val Ile Ile His Glu Val Lys Ile Asn Val Ser Pro  
 385                                      390                                      395                                      400  
 Gly Tyr Ser Phe His Cys Thr Glu Pro Gly Trp Phe Arg Val Cys Tyr  
                                     405                                      410                                      415  
 Ala Asn Met Asp Asp Met Ala Val Gln Ile Ala Leu Gln Arg Ile Arg  
                                     420                                      425                                      430  
 Asn Phe Val Leu Gln Asn Lys Glu Val Val Val Ser Asn Lys Lys His  
                                     435                                      440                                      445  
 Cys Trp His Ser Asn Leu Arg Leu Ser Leu Lys Thr Arg Arg Phe Asp  
                                     450                                      455                                      460  
 Asp Ile Thr Met Ser Pro His Ser Pro Leu Pro Gln Ser Pro Met Val  
 465                                      470                                      475                                      480  
 Lys Ala Thr Asn

&lt;210&gt; 3

&lt;211&gt; 2474

&lt;212&gt; DNA

&lt;213&gt; Plant

&lt;400&gt; 3

ttacagatac acagaatcag acgacacatc tactttaata acagaaaaat aataagtgtc 60

- 7 -

ggagattatg gtacgacaag atgaaatggt tttatatggt tgagattatt ttgggtctggt 120  
gttggaagtt tcacgaatca tgattttgat tttacgtatt aaaaaatgaa aagttgaatc 180  
atgcatttta tctagaagct gggaactgaa ccaaaaaaat agccagttga acaactgcag 240  
tatttgtagg cgtattcatt tctcctttcc tacaataatc cttgggttget ctttatcgga 300  
aaaaaaccaa aagcaatagc tactctgtaa ggtcctcgat tgccgacaag aacatcacat 360  
gcgtgctgic gaagaacaca taattttgag gttgaagctc acgtgcgagt tttgcatatt 420  
tttaggttat gtgtacacgt atggagttag ttccgcgtat atagtgtagg tagttgagtg 480  
gctgagtagc gagtgaatca ggtaacacta tcttttcaag ccacctaatt aagggattta 540  
atgttcatgc aactgttctt cgctaactaa ggccccactt acctttataa tattctctct 600  
aactccgggc ttttggtgag tacaactttt ctactcttat ttaatggagg gattatcttt 660  
tccatatacc aattaattta ttttttaatt tatgcatttt gatcttatat taaaacaatt 720  
atggtatgga ttaagtcgta ttcggtgac aattgaagtt ttcctcaagt ttagccattt 780  
ttatgaaatt aaacttaatc actactatta ggtaaatcca tatgtatcat taacaatttc 840  
aatgtgagtt caattttacc caagatttga aagttgttgt caacttctgt taactaaagt 900  
tgtattataa ggttgacgac tttaacctaa atctatcttg aattgaaggg gttgatgact 960  
tcagctttta aataattcaa cttaaagttct agactacatt ggagatttta gtgttcataa 1020  
aattttagaa aaaggctgag ttaaagttat gaaaaagatt ggtgactatt caattaatta 1080  
gttgtgaatt gatgacaaat atttcatgag cataaccaat cagagaaata ccacctcgac 1140  
cgactacaac aatctcaatg ttaattaatg aagcattgta gtataaggag tctagaataa 1200  
atctcttaaa tattagagga aaactatctt taaaaaatta caagaaaagt ttgatctata 1260  
acctctttta acttttaatt atctaacaat tttcttatga ctcacattgt gttgataggg 1320  
tgattttgtc aaaatatatg tctatcttat actagtatga tttgtctgag aattatatat 1380  
agtattaact tggagaaatg attgcctaatt aagttataaa aaaggagaaa atatttatct 1440

- 8 -

ataaaaaaaa tacacttaaa taagtaacaa taataaaaaa cattatataa gagattaaga 1500  
 taatttaata agtattgaat gtagaataat ttttatttat aaatttgaac taaaatattc 1560  
 aaataatatt caaagtaaat aatagatata attcatcatt caatacgagt aattcaatct 1620  
 attataatca tatattagat aaatatacaa atatttgta aattttacat tattatatta 1680  
 ctaaataatatt attaatttct ttgaatatct tttatacaag taggtagact agaagaatta 1740  
 tcttatctcc cgtatatttg tagatgtaa atgtaacggg ctttagactga tgtttttgta 1800  
 ttatattatt tataaatcca ttagagattt aagttaatgt ctctcttga ttttaacatg 1860  
 gttctaaaaa ttaggttaa tcattgcgtc ctcaatgaac ccatgctata tgttttaaag 1920  
 ttttttggtt ttgacaatg ttttttattt ctgagattgc tcttaggatt gaaattatgt 1980  
 ttgatactag aaaacgaaga agtagagagt agtgatata cgtgtaaaaa ataatagttg 2040  
 tgggaactta agttggattt gaatactagg acgaggctgg aagggtttcc actaagttga 2100  
 caaaaattat tacaagtggc aactagctag gtctcacaaa gtattactaa ttaatagttg 2160  
 gtctgtctgc ataccaactc ttgctaatt ttcaaacacc gcattctctc ttcttctctc 2220  
 cttcttctc tggaaactc atcgatgtgg acttctgtct ctcaaagtc aagctcaatt 2280  
 tatccaatgc attataaata cacactctcc ctcccttcta ttcttcattg catcacattt 2340  
 cctctataaa ttactcacac cttattccta acttcatttc aacatcctct ctcccactta 2400  
 cttcgatttc atcaattcca ataaactcaa cacacttttt tacaactccac actctaacca 2460  
 catacaccat atgg

2474

<210> 4  
 <211> 29  
 <212> DNA  
 <213> Plant

<400> 4  
 gcggatccat cttggacaac aaggagtt



- 9 -

<210> 5  
<211> 30  
<212> DNA  
<213> Plant

<400> 5  
taggatccag aaagacactg agaaccgtgg

30

<210> 6  
<211> 29  
<212> DNA  
<213> Plant

<400> 6  
acggatccgg tgtatgtggt tagagtgtg

29

<210> 7  
<211> 29  
<212> DNA  
<213> Plant

<400> 7  
caggatccag acatagagtg tgaccgcaa

29

<210> 8  
<211> 59  
<212> DNA  
<213> Plant

<400> 8  
atcgatcata tgagctctag acccgggctg caggatccgg tgtatgtggt tagagtgtg

59

<210> 9  
<211> 57  
<212> DNA  
<213> Plant

<400> 9  
ccgcggagat ctatcgatct cgagaattca agcttcagac atagagtgtg accgcaa

57